



#7

SEQUENCE LISTING

<110> David, Sanders A

Richard, Kuhn John

Scott, Jeffers A

Curtis, Sharkey Matthew

Cynthia, North Lin

Michael, Fishbach A

<120> Pseudotyped Retroviruses and Stable Cell Lines For Their
Production

<130> 3220-69199

<140> 09/762,224

<141> 2001-02-02

<150> PCT/US99/17702

<151> 1999-08-04

<150> US 60/112,405

<151> 1998-12-15

<150> US 60/095,242

<151> 1998-08-04

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 2958

<212> DNA

<213> Ross River virus

<220>

<221> CDS

<222> (1)..(2955)

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Cys Ser Ser Pro Pro Cys Tyr Pro Cys Cys Tyr Glu Lys Gln Pro Glu	
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cag aca ctg cgg atg ctg gaa gac aat gtg aat aga cca ggg tac tat	144
Gln Thr Leu Arg Met Leu Glu Asp Asn Val Asn Arg Pro Gly Tyr Tyr	
35 40 45	
gag cta ctg gaa gcg tcc atg aca tgc aga aac aga tca cgc cac cgc	192
Glu Leu Leu Glu Ala Ser Met Thr Cys Arg Asn Arg Ser Arg His Arg	
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cgt agt gta aca gag cac ttc aat gtg tat aag gct act aga ccg tac	240
Arg Ser Val Thr Glu His Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr	
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Leu Ala Tyr Cys Ala Asp Cys Gly Asp Gly Tyr Phe Cys Tyr Ser Pro	
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ggt gct atc gag aag atc cga gat gag gcg tct gac ggc atg ctc aag	336
Val Ala Ile Glu Lys Ile Arg Asp Glu Ala Ser Asp Gly Met Leu Lys	
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atc caa gtc tcc gcc caa ata ggt ctg gac aag gca ggt acc cac gcc	384
Ile Gln Val Ser Ala Gln Ile Gly Leu Asp Lys Ala Gly Thr His Ala	
115 120 125	
cac acg aag atc cga tat atg gct ggt cat gat gtt cag gaa tct aag	432
His Thr Lys Ile Arg Tyr Met Ala Gly His Asp Val Gln Glu Ser Lys	
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aga gat tcc ttg agg gtg tac acg tcc gca gcg tgc tct ata cat ggg	480
Arg Asp Ser Leu Arg Val Tyr Thr Ser Ala Ala Cys Ser Ile His Gly	
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Thr Met Gly His Phe Ile Val Ala His Cys Pro Pro Gly Asp Tyr Leu	
165 170 175	
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Lys Val Ser Phe Glu Asp Ala Asp Ser His Val Lys Ala Cys Lys Val	
180 185 190	
caa tac aag cac gac cca ttg ccg gtg ggt aga gag aag ttc gtg gtt	624
Gln Tyr Lys His Asp Pro Leu Pro Val Gly Arg Glu Lys Phe Val Val	
195 200 205	
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Arg Pro His Phe Gly Val Glu Leu Pro Cys Thr Ser Tyr Gln Leu Thr	
210 215 220	
aca gct ccc acc gac gag gag atc gac atg cac aca ccg cca gat ata	720
Thr Ala Pro Thr Asp Glu Glu Ile Asp Met His Thr Pro Pro Asp Ile	
225 230 235 240	
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Pro Asp Arg Thr Leu Leu Ser Gln Thr Ala Gly Asn Val Lys Ile Thr	
245 250 255	
gca ggc ggc agg act atc agg tac aat tgt acc tgt ggc cgt gac aac	816
Ala Gly Gly Arg Thr Ile Arg Tyr Asn Cys Thr Cys Gly Arg Asp Asn	
260 265 270	

gta ggc act acc agt act gac aag acc atc aac aca tgc aag att gac	864
Val Gly Thr Thr Ser Thr Asp Lys Thr Ile Asn Thr Cys Lys Ile Asp	
275 280 285	
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Gln Cys His Ala Ala Val Thr Ser His Asp Lys Trp Gln Phe Thr Ser	
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Pro Phe Val Pro Arg Ala Asp Gln Thr Ala Arg Arg Gly Lys Val His	
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Val Pro Phe Pro Leu Thr Asn Val Thr Cys Arg Val Pro Leu Ala Arg	
325 330 335	
gcg ccg gat gtc acc tat ggt aag aag gag gtg acc ctg aga tta cac	1056
Ala Pro Asp Val Thr Tyr Gly Lys Lys Glu Val Thr Leu Arg Leu His	
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cca gat cat ccg acg ctc ttc tcc tat agg agt tta gga gcc gaa ccg	1104
Pro Asp His Pro Thr Leu Phe Ser Tyr Arg Ser Leu Gly Ala Glu Pro	
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cac ccg tac gag gag tgg gtt gac aag ttc tct gag cgc atc atc cca	1152
His Pro Tyr Glu Glu Trp Val Asp Lys Phe Ser Glu Arg Ile Ile Pro	
370 375 380	
gtg acg gaa gaa ggg att gag tac cag tgg ggc aac aac ccg ccg gtc	1200
Val Thr Glu Glu Gly Ile Glu Tyr Gln Trp Gly Asn Asn Pro Pro Val	
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Arg Leu Trp Ala Gln Leu Thr Thr Glu Gly Lys Pro His Gly Trp Pro	
405 410 415	
cat gaa atc att cag tac tat tat gga cta tac ccc gcc gcc acc att	1296
His Glu Ile Ile Gln Tyr Tyr Tyr Gly Leu Tyr Pro Ala Ala Thr Ile	
420 425 430	
gcc gca gta tcc ggg gcg agt ctg atg gcc ctc cta act cta gcg gcc	1344
Ala Ala Val Ser Gly Ala Ser Leu Met Ala Leu Leu Thr Leu Ala Ala	
435 440 445	
aca tgc tgc atg ctg gcc acc gcg agg aga aag tgc cta aca cca tac	1392
Thr Cys Cys Met Leu Ala Thr Ala Arg Arg Lys Cys Leu Thr Pro Tyr	
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Ala Leu Thr Pro Gly Ala Val Val Pro Leu Thr Leu Gly Leu Leu Cys	
465 470 475 480	
tgc gca ccg agg gcg aac gca gca tca ttc gct gag act atg gca tat	1488
Cys Ala Pro Arg Ala Asn Ala Ala Ser Phe Ala Glu Thr Met Ala Tyr	
485 490 495	
ctg tgg gac gag aac aaa acc ctc ttt tgg atg gaa ttc gcc gcc cca	1536
Leu Trp Asp Glu Asn Lys Thr Leu Phe Trp Met Glu Phe Ala Ala Pro	
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gcc gca gcg ctt gct ttg ctg gca tgc tgt atc aaa agc ctg atc tgc	1584
Ala Ala Ala Leu Ala Leu Leu Ala Cys Cys Ile Lys Ser Leu Ile Cys	
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Cys Cys Lys Pro Phe Ser Phe Leu Val Leu Leu Ser Leu Gly Ala Ser	
530 535 540	
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Ala Lys Ala Tyr Glu His Thr Ala Thr Ile Pro Asn Val Val Gly Phe	
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Pro Tyr Lys Ala His Ile Glu Arg Asn Gly Phe Ser Pro Met Thr Leu	
565 570 575	
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Gln Leu Glu Val Val Glu Thr Ser Leu Glu Pro Thr Leu Asn Leu Glu	
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tac att acc tgc gaa tac aag acg gtg gtc cct tcg cca ttc atc aaa	1824
Tyr Ile Thr Cys Glu Tyr Lys Thr Val Val Pro Ser Pro Phe Ile Lys	
595 600 605	
tgt tgc gga aca tca gaa tgc tca tcc aag gag cag cca gac tac caa	1872
Cys Cys Gly Thr Ser Glu Cys Ser Ser Lys Glu Gln Pro Asp Tyr Gln	
610 615 620	
tgc aag gtg tac acg ggt gta tac cca ttc atg tgg ggt gga gcc tac	1920
Cys Lys Val Tyr Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr	
625 630 635 640	
tgt ttc tgc gac tcc gag aac acg cag ctc agc gag gcc tat gtc gac	1968
Cys Phe Cys Asp Ser Glu Asn Thr Gln Leu Ser Glu Ala Tyr Val Asp	
645 650 655	

agg tca gac gtt tgc aaa cat gat cac gca tcg gcc tac aag gca cac	2016
Arg Ser Asp Val Cys Lys His Asp His Ala Ser Ala Tyr Lys Ala His	
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acg gcc tct cta aaa gca aca atc agg atc agt tat ggc acc atc aac	2064
Thr Ala Ser Leu Lys Ala Thr Ile Arg Ile Ser Tyr Gly Thr Ile Asn	
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Gln Thr Thr Glu Ala Phe Val Asn Gly Glu His Ala Val Asn Val Gly	
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Gly Ser Lys Phe Ile Phe Gly Pro Ile Ser Thr Ala Trp Ser Pro Phe	
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Asp Asn Lys Ile Val Val Tyr Lys Asp Asp Val Tyr Asn Gln Asp Phe	
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cca ccc tac gga tca ggc cag ccg ggt aga ttc gga gac att cag agc	2256
Pro Pro Tyr Gly Ser Gly Gln Pro Gly Arg Phe Gly Asp Ile Gln Ser	
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Arg Thr Val Glu Ser Lys Asp Leu Tyr Ala Asn Thr Ala Leu Lys Leu	
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Ser Arg Pro Ser Pro Gly Val Val His Val Pro Tyr Thr Gln Thr Pro	
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Ser Gly Phe Lys Tyr Trp Leu Lys Glu Lys Gly Ser Ser Leu Asn Thr	
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aag gcc cct ttt ggc tgc aag ata aag acc aat cca gtc aga gcc atg	2448
Lys Ala Pro Phe Gly Cys Lys Ile Lys Thr Asn Pro Val Arg Ala Met	
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gat tgt gca gtt ggc agt ata cct gtg tcg atg gac ata cct gac agt	2496
Asp Cys Ala Val Gly Ser Ile Pro Val Ser Met Asp Ile Pro Asp Ser	
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Ala Phe Thr Arg Val Val Asp Ala Pro Ala Val Thr Asp Leu Ser Cys	
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Gln Val Val Val Cys Thr His Ser Ser Asp Phe Gly Gly Val Ala Thr	
850 855 860	
ttg tct tac aaa acg gac aaa ccc ggc aag tgc gct gtc cac tca cat	2640
Leu Ser Tyr Lys Thr Asp Lys Pro Gly Lys Cys Ala Val His Ser His	
865 870 875 880	
tcc aac gtc gca acg ttg caa gag gcg acg gtg gat gtc aag gag gat	2688
Ser Asn Val Ala Thr Leu Gln Glu Ala Thr Val Asp Val Lys Glu Asp	
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ggc aag gtc aca gtg cac ttt tcc acg gcg tcc gcc tcc ccg gcc ttc	2736
Gly Lys Val Thr Val His Phe Ser Thr Ala Ser Ala Ser Pro Ala Phe	
900 905 910	
aaa gtg tcc gtc tgt gac gca aaa aca acg tgc acg gcg gcg tgc gag	2784
Lys Val Ser Val Cys Asp Ala Lys Thr Thr Cys Thr Ala Ala Cys Glu	
915 920 925	
cct cca aaa gac cac atc gtc cct tat ggg gcg agc cat aac aac cag	2832
Pro Pro Lys Asp His Ile Val Pro Tyr Gly Ala Ser His Asn Asn Gln	
930 935 940	
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Val Phe Pro Asp Met Ser Gly Thr Ala Met Thr Trp Val Gln Arg Leu	
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Ala Ser Gly Leu Gly Gly Leu Ala Leu Ile Ala Val Val Val Leu Val	
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<212> PRT

<213> Ross River virus

<400> 2

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Gln Thr Leu Arg Met Leu Glu Asp Asn Val Asn Arg Pro Gly Tyr Tyr
 35 40 45

Glu Leu Leu Glu Ala Ser Met Thr Cys Arg Asn Arg Ser Arg His Arg
 50 55 60

Arg Ser Val Thr Glu His Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr
 65 70 75 80

Leu Ala Tyr Cys Ala Asp Cys Gly Asp Gly Tyr Phe Cys Tyr Ser Pro
 85 90 95

Val Ala Ile Glu Lys Ile Arg Asp Glu Ala Ser Asp Gly Met Leu Lys
 100 105 110

Ile Gln Val Ser Ala Gln Ile Gly Leu Asp Lys Ala Gly Thr His Ala
 115 120 125

His Thr Lys Ile Arg Tyr Met Ala Gly His Asp Val Gln Glu Ser Lys
 130 135 140

Arg Asp Ser Leu Arg Val Tyr Thr Ser Ala Ala Cys Ser Ile His Gly
 145 150 155 160

Thr Met Gly His Phe Ile Val Ala His Cys Pro Pro Gly Asp Tyr Leu
 165 170 175

Lys Val Ser Phe Glu Asp Ala Asp Ser His Val Lys Ala Cys Lys Val
 180 185 190

Gln Tyr Lys His Asp Pro Leu Pro Val Gly Arg Glu Lys Phe Val Val
 195 200 205

Arg Pro His Phe Gly Val Glu Leu Pro Cys Thr Ser Tyr Gln Leu Thr
 210 215 220

Thr Ala Pro Thr Asp Glu Glu Ile Asp Met His Thr Pro Pro Asp Ile
 225 230 235 240

Pro Asp Arg Thr Leu Leu Ser Gln Thr Ala Gly Asn Val Lys Ile Thr
 245 250 255

Ala Gly Gly Arg Thr Ile Arg Tyr Asn Cys Thr Cys Gly Arg Asp Asn
 260 265 270

Val Gly Thr Thr Ser Thr Asp Lys Thr Ile Asn Thr Cys Lys Ile Asp
 275 280 285

Gln Cys His Ala Ala Val Thr Ser His Asp Lys Trp Gln Phe Thr Ser
 290 295 300

Pro Phe Val Pro Arg Ala Asp Gln Thr Ala Arg Arg Gly Lys Val His
 305 310 315 320

Val Pro Phe Pro Leu Thr Asn Val Thr Cys Arg Val Pro Leu Ala Arg
 325 330 335

Ala Pro Asp Val Thr Tyr Gly Lys Lys Glu Val Thr Leu Arg Leu His
 340 345 350

Pro Asp His Pro Thr Leu Phe Ser Tyr Arg Ser Leu Gly Ala Glu Pro
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His Pro Tyr Glu Glu Trp Val Asp Lys Phe Ser Glu Arg Ile Ile Pro
 370 375 380

Val Thr Glu Glu Gly Ile Glu Tyr Gln Trp Gly Asn Asn Pro Pro Val
 385 390 395 400

Arg Leu Trp Ala Gln Leu Thr Thr Glu Gly Lys Pro His Gly Trp Pro
 405 410 415

His Glu Ile Ile Gln Tyr Tyr Tyr Gly Leu Tyr Pro Ala Ala Thr Ile
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Ala Ala Val Ser Gly Ala Ser Leu Met Ala Leu Leu Thr Leu Ala Ala
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Ala Leu Thr Pro Gly Ala Val Val Pro Leu Thr Leu Gly Leu Leu Cys
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Cys Ala Pro Arg Ala Asn Ala Ala Ser Phe Ala Glu Thr Met Ala Tyr
 485 490 495

Leu Trp Asp Glu Asn Lys Thr Leu Phe Trp Met Glu Phe Ala Ala Pro
 500 505 510

Ala Ala Ala Leu Ala Leu Leu Ala Cys Cys Ile Lys Ser Leu Ile Cys
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Cys Cys Lys Pro Phe Ser Phe Leu Val Leu Leu Ser Leu Gly Ala Ser
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Pro Tyr Lys Ala His Ile Glu Arg Asn Gly Phe Ser Pro Met Thr Leu
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580 585 590

Tyr Ile Thr Cys Glu Tyr Lys Thr Val Val Pro Ser Pro Phe Ile Lys
595 600 605

Cys Cys Gly Thr Ser Glu Cys Ser Ser Lys Glu Gln Pro Asp Tyr Gln
610 615 620

Cys Lys Val Tyr Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr
625 630 635 640

Cys Phe Cys Asp Ser Glu Asn Thr Gln Leu Ser Glu Ala Tyr Val Asp
645 650 655

Arg Ser Asp Val Cys Lys His Asp His Ala Ser Ala Tyr Lys Ala His
660 665 670

Thr Ala Ser Leu Lys Ala Thr Ile Arg Ile Ser Tyr Gly Thr Ile Asn
675 680 685

Gln Thr Thr Glu Ala Phe Val Asn Gly Glu His Ala Val Asn Val Gly
690 695 700

Gly Ser Lys Phe Ile Phe Gly Pro Ile Ser Thr Ala Trp Ser Pro Phe
705 710 715 720

Asp Asn Lys Ile Val Val Tyr Lys Asp Asp Val Tyr Asn Gln Asp Phe
725 730 735

Pro Pro Tyr Gly Ser Gly Gln Pro Gly Arg Phe Gly Asp Ile Gln Ser
740 745 750

Arg Thr Val Glu Ser Lys Asp Leu Tyr Ala Asn Thr Ala Leu Lys Leu
755 760 765

Ser Arg Pro Ser Pro Gly Val Val His Val Pro Tyr Thr Gln Thr Pro
 770 775 780

Ser Gly Phe Lys Tyr Trp Leu Lys Glu Lys Gly Ser Ser Leu Asn Thr
 785 790 795 800

Lys Ala Pro Phe Gly Cys Lys Ile Lys Thr Asn Pro Val Arg Ala Met
 805 810 815

Asp Cys Ala Val Gly Ser Ile Pro Val Ser Met Asp Ile Pro Asp Ser
 820 825 830

Ala Phe Thr Arg Val Val Asp Ala Pro Ala Val Thr Asp Leu Ser Cys
 835 840 845

Gln Val Val Val Cys Thr His Ser Ser Asp Phe Gly Gly Val Ala Thr
 850 855 860

Leu Ser Tyr Lys Thr Asp Lys Pro Gly Lys Cys Ala Val His Ser His
 865 870 875 880

Ser Asn Val Ala Thr Leu Gln Glu Ala Thr Val Asp Val Lys Glu Asp
 885 890 895

Gly Lys Val Thr Val His Phe Ser Thr Ala Ser Ala Ser Pro Ala Phe
 900 905 910

Lys Val Ser Val Cys Asp Ala Lys Thr Thr Cys Thr Ala Ala Cys Glu
 915 920 925

Pro Pro Lys Asp His Ile Val Pro Tyr Gly Ala Ser His Asn Asn Gln
 930 935 940

Val Phe Pro Asp Met Ser Gly Thr Ala Met Thr Trp Val Gln Arg Leu
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Leu Val Thr Cys Ile Thr Met Arg Arg
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<212> DNA

<213> Ebola virus

<220>

<221> CDS

<222> (11)..(2038)

<223>

<400> 3

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 Phe Lys Arg Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg
 15 20 25

aca ttt tcc atc cca ctt gga gtc atc cac aat agc aca tta cag gtt 145
 Thr Phe Ser Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val
 30 35 40 45

agt gat gtc gac aaa cta gtt tgt cgt gac aaa ctg tca tcc aca aat 193
 Ser Asp Val Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn
 50 55 60

caa ttg aga tca gtt gga ctg aat ctc gaa ggg aat gga gtg gca act 241
 Gln Leu Arg Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr
 65 70 75

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cca	aag	gtg	gtc	aat	tat	gaa	gct	ggg	gaa	tgg	gct	gaa	aac	tgc	tac	337
Pro	Lys	Val	Val	Asn	Tyr	Glu	Ala	Gly	Glu	Trp	Ala	Glu	Asn	Cys	Tyr	
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aat	ctt	gaa	atc	aaa	aaa	cct	gac	ggg	agt	gag	tgt	cta	cca	gca	gcg	385
Asn	Leu	Glu	Ile	Lys	Lys	Pro	Asp	Gly	Ser	Glu	Cys	Leu	Pro	Ala	Ala	
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cca	gac	ggg	att	cgg	ggc	ttc	ccc	cgg	tgc	cgg	tat	gtg	cac	aaa	gta	433
Pro	Asp	Gly	Ile	Arg	Gly	Phe	Pro	Arg	Cys	Arg	Tyr	Val	His	Lys	Val	
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tca	gga	acg	gga	ccg	tgt	gcc	gga	gac	ttt	gcc	ttc	cat	aaa	gag	ggg	481
Ser	Gly	Thr	Gly	Pro	Cys	Ala	Gly	Asp	Phe	Ala	Phe	His	Lys	Glu	Gly	
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gct	ttc	ttc	ctg	tat	gat	cga	ctt	gct	tcc	aca	gtt	atc	tac	cga	gga	529
Ala	Phe	Phe	Leu	Tyr	Asp	Arg	Leu	Ala	Ser	Thr	Val	Ile	Tyr	Arg	Gly	
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acg	act	ttc	gct	gaa	ggg	gtc	gtt	gca	ttt	ctg	ata	ctg	ccc	caa	gct	577
Thr	Thr	Phe	Ala	Glu	Gly	Val	Val	Ala	Phe	Leu	Ile	Leu	Pro	Gln	Ala	
	175					180					185					
aag	aag	gac	ttc	ttc	agc	tca	cac	ccc	ttg	aga	gag	ccg	gtc	aat	gca	625
Lys	Lys	Asp	Phe	Phe	Ser	Ser	His	Pro	Leu	Arg	Glu	Pro	Val	Asn	Ala	
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acg	gag	gac	ccg	tct	agt	ggc	tac	tat	tct	acc	aca	att	aga	tat	cag	673
Thr	Glu	Asp	Pro	Ser	Ser	Gly	Tyr	Tyr	Ser	Thr	Thr	Ile	Arg	Tyr	Gln	
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gct	acc	ggg	ttt	gga	acc	aat	gag	aca	gag	tac	ttg	ttc	gag	gtt	gac	721
Ala	Thr	Gly	Phe	Gly	Thr	Asn	Glu	Thr	Glu	Tyr	Leu	Phe	Glu	Val	Asp	
			225					230					235			
aat	ttg	acc	tac	gtc	caa	ctt	gaa	tca	aga	ttc	aca	cca	cag	ttt	ctg	769
Asn	Leu	Thr	Tyr	Val	Gln	Leu	Glu	Ser	Arg	Phe	Thr	Pro	Gln	Phe	Leu	
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ctc	cag	ctg	aat	gag	aca	ata	tat	aca	agt	ggg	aaa	agg	agc	aat	acc	817
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ggg gag tgg gcc ttc tgg gaa act aaa aaa aac ctc act aga aaa att	913
Gly Glu Trp Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile	
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cgc agt gaa gag ttg tct ttc aca gtt gta tca aac gga gcc aaa aac	961
Arg Ser Glu Glu Leu Ser Phe Thr Val Val Ser Asn Gly Ala Lys Asn	
305 310 315	
atc agt ggt cag agt ccg gcg cga act tct tcc gac cca ggg acc aac	1009
Ile Ser Gly Gln Ser Pro Ala Arg Thr Ser Ser Asp Pro Gly Thr Asn	
320 325 330	
aca aca act gaa gac cac aaa atc atg gct tca gaa aat tcc tct gca	1057
Thr Thr Thr Glu Asp His Lys Ile Met Ala Ser Glu Asn Ser Ser Ala	
335 340 345	
atg gtt caa gtg cac agt caa gga agg gaa gct gca gtg tcg cat cta	1105
Met Val Gln Val His Ser Gln Gly Arg Glu Ala Ala Val Ser His Leu	
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aca acc ctt gcc aca atc tcc acg agt ccc caa tcc ctc aca acc aaa	1153
Thr Thr Leu Ala Thr Ile Ser Thr Ser Pro Gln Ser Leu Thr Thr Lys	
370 375 380	
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Pro Gly Pro Asp Asn Ser Thr His Asn Thr Pro Val Tyr Lys Leu Asp	
385 390 395	
atc tct gag gca act caa gtt gaa caa cat cac cgc aga aca gac aac	1249
Ile Ser Glu Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn	
400 405 410	
gac agc aca gcc tcc gac act ccc tct gcc acg acc gca gcc gga ccc	1297
Asp Ser Thr Ala Ser Asp Thr Pro Ser Ala Thr Thr Ala Ala Gly Pro	
415 420 425	
cca aaa gca gag aac acc aac acg agc aag agc act gac ttc ctg gac	1345
Pro Lys Ala Glu Asn Thr Asn Thr Ser Lys Ser Thr Asp Phe Leu Asp	
430 435 440 445	
ccc gcc acc aca aca agt ccc caa aac cac agc gag acc gct ggc aac	1393
Pro Ala Thr Thr Thr Ser Pro Gln Asn His Ser Glu Thr Ala Gly Asn	
450 455 460	

aac aac act cat cac caa gat acc gga gaa gag agt gcc agc agc ggg	1441
Asn Asn Thr His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly	
465 470 475	
aag cta ggc tta att acc aat act att gct gga gtc gca gga ctg atc	1489
Lys Leu Gly Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile	
480 485 490	
aca ggc ggg aga aga act cga aga gaa gca att gtc aat gct caa ccc	1537
Thr Gly Gly Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro	
495 500 505	
aaa tgc aac cct aat tta cat tac tgg act act cag gat gaa ggt gct	1585
Lys Cys Asn Pro Asn Leu His Tyr Trp Thr Thr Gln Asp Glu Gly Ala	
510 515 520 525	
gca atc gga ctg gcc tgg ata cca tat ttc ggg cca gca gcc gag gga	1633
Ala Ile Gly Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly	
530 535 540	
att tac ata gag ggg cta atg cac aat caa gat ggt tta atc tgt ggg	1681
Ile Tyr Ile Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly	
545 550 555	
ttg aga cag ctg gcc aac gag acg act caa gct ctt caa ctg ttc ctg	1729
Leu Arg Gln Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu	
560 565 570	
aga gcc aca act gag cta cgc acc ttt tca atc ctc aac cgt aag gca	1777
Arg Ala Thr Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala	
575 580 585	
att gat ttc ttg ctg cag cga tgg ggc ggc aca tgc cac att ctg gga	1825
Ile Asp Phe Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly	
590 595 600 605	
ccg gac tgc tgt atc gaa cca cat gat tgg acc aag aac ata aca gac	1873
Pro Asp Cys Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp	
610 615 620	
aaa att gat cag att att cat gat ttt gtt gat aaa acc ctt ccg gac	1921
Lys Ile Asp Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp	
625 630 635	
cag ggg gac aat gac aat tgg tgg aca gga tgg aga caa tgg ata ccg	1969
Gln Gly Asp Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro	
640 645 650	

gca ggt att gga gtt aca ggc gtt ata att gca gtt atc gct tta ttc 2017
 Ala Gly Ile Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe
 655 660 665

tgt ata tgc aaa ttt gtc ttt tagtttttct tcagattgct tcatggaaaa 2068
 Cys Ile Cys Lys Phe Val Phe
 670 675

gctcagcctc aaatcaatga aaccaggatt taattatatg gattacttga atctaagatt 2128

acttgacaaa tgataatata atacactgga gcttttaaaca tagccaatgt gattctaact 2188

ccttttaaact cacagttaat cataaacaag gtttga 2224

<210> 4

<211> 676

<212> PRT

<213> Ebola virus

<400> 4

Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys Arg
 1 5 10 15

Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe Ser
 20 25 30

Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp Val
 35 40 45

Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu Arg
 50 55 60

Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val Pro
 65 70 75 80

Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val
 85 90 95

Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
100 105 110

Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp Gly
115 120 125

Ile Arg Gly Phe Pro Arg Cys Arg Tyr Val His Lys Val Ser Gly Thr
130 135 140

Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe Phe
145 150 155 160

Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr Phe
165 170 175

Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys Asp
180 185 190

Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu Asp
195 200 205

Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr Gly
210 215 220

Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu Thr
225 230 235 240

Tyr Val Gln Leu Glu Ser Arg Phe Thr Pro Gln Phe Leu Leu Gln Leu
245 250 255

Asn Glu Thr Ile Tyr Thr Ser Gly Lys Arg Ser Asn Thr Thr Gly Lys
260 265 270

Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu Trp
275 280 285

Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser Glu
290 295 300

Glu Leu Ser Phe Thr Val Val Ser Asn Gly Ala Lys Asn Ile Ser Gly
305 310 315 320

Gln Ser Pro Ala Arg Thr Ser Ser Asp Pro Gly Thr Asn Thr Thr Thr
325 330 335

Glu Asp His Lys Ile Met Ala Ser Glu Asn Ser Ser Ala Met Val Gln
340 345 350

Val His Ser Gln Gly Arg Glu Ala Ala Val Ser His Leu Thr Thr Leu
355 360 365

Ala Thr Ile Ser Thr Ser Pro Gln Ser Leu Thr Thr Lys Pro Gly Pro
370 375 380

Asp Asn Ser Thr His Asn Thr Pro Val Tyr Lys Leu Asp Ile Ser Glu
385 390 395 400

Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn Asp Ser Thr
405 410 415

Ala Ser Asp Thr Pro Ser Ala Thr Thr Ala Ala Gly Pro Pro Lys Ala
420 425 430

Glu Asn Thr Asn Thr Ser Lys Ser Thr Asp Phe Leu Asp Pro Ala Thr
435 440 445

Thr Thr Ser Pro Gln Asn His Ser Glu Thr Ala Gly Asn Asn Asn Thr
450 455 460

His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu Gly
465 470 475 480

Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly Gly
485 490 495

Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys Asn
500 505 510

Pro Asn Leu His Tyr Trp Thr Thr Gln Asp Glu Gly Ala Ala Ile Gly
515 520 525

Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr Ile
530 535 540

Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg Gln
545 550 555 560

Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr
565 570 575

Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp Phe
580 585 590

Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp Cys
595 600 605

Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile Asp
610 615 620

Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly Asp
625 630 635 640

Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly Ile
645 650 655

Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe Cys Ile Cys
660 665 670

Lys Phe Val Phe
675

<210> 5

<211> 2103

<212> DNA

<213> Marburg virus

<220>

<221> CDS

<222> (10)..(2052)

<223>

<400> 5

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	Met	Lys	Thr	Thr	Cys	Phe	Leu	Ile	Ser	Leu	Ile	Leu	Ile	Gln	
	1				5					10					

ggg	aca	aaa	aat	ctc	ccc	att	tta	gag	ata	gct	agt	aat	aat	caa	ccc	99
Gly	Thr	Lys	Asn	Leu	Pro	Ile	Leu	Glu	Ile	Ala	Ser	Asn	Asn	Gln	Pro	
15				20				25						30		

caa	aat	gtg	gat	tcg	gta	tgc	tcc	gga	act	ctc	cag	aag	aca	gaa	gac	147
Gln	Asn	Val	Asp	Ser	Val	Cys	Ser	Gly	Thr	Leu	Gln	Lys	Thr	Glu	Asp	
				35				40						45		

gtc	cat	ctg	atg	gga	ttc	aca	ctg	agt	ggg	caa	aaa	gtt	gct	gat	tcc	195
Val	His	Leu	Met	Gly	Phe	Thr	Leu	Ser	Gly	Gln	Lys	Val	Ala	Asp	Ser	
			50				55					60				

cct	ttg	gag	gca	tcc	aag	cga	tgg	gct	ttc	agg	aca	ggg	gta	cct	ccc	243
Pro	Leu	Glu	Ala	Ser	Lys	Arg	Trp	Ala	Phe	Arg	Thr	Gly	Val	Pro	Pro	
		65					70					75				

aag	aat	gtt	gag	tac	aca	gag	ggg	gag	gaa	gcc	aaa	aca	tgc	tac	aat	291
Lys	Asn	Val	Glu	Tyr	Thr	Glu	Gly	Glu	Glu	Ala	Lys	Thr	Cys	Tyr	Asn	
	80					85					90					

ata agt gta acg gat ccc tct gga aaa tcc ttg ctg tta gat cct cct	339
Ile Ser Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro	
95 100 105 110	
acc aac atc cgt gac tat cct aaa tgc aaa act atc cat cat att caa	387
Thr Asn Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln	
115 120 125	
ggg caa aac cct cat gca cag ggg atc gcc ctt cat tta tgg gga gca	435
Gly Gln Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala	
130 135 140	
ttt ttt ctg tat gat cgc att gcc tcc aca aca atg tac cga ggc aaa	483
Phe Phe Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys	
145 150 155	
gtc ttc act gaa ggg aac ata gca gct atg att gtc aat aag aca gtg	531
Val Phe Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val	
160 165 170	
cac aaa atg att ttc tcg cgg caa gga caa ggg tac cgt cat atg aat	579
His Lys Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn	
175 180 185 190	
ctg act tct act aat aaa tat tgg aca agt agt aac gga acg caa acg	627
Leu Thr Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr	
195 200 205	
aat gac act gga tgt ttc ggc gct ctt caa gaa tac aat tct aca aag	675
Asn Asp Thr Gly Cys Phe Gly Ala Leu Gln Glu Tyr Asn Ser Thr Lys	
210 215 220	
aac caa aca tgt gct ccg tcc aaa ata cct cca cca ctg ccc aca gcc	723
Asn Gln Thr Cys Ala Pro Ser Lys Ile Pro Pro Pro Leu Pro Thr Ala	
225 230 235	
cgt ccg gag atc aaa ctc aca agc acc cca act gat gcc acc aaa ctc	771
Arg Pro Glu Ile Lys Leu Thr Ser Thr Pro Thr Asp Ala Thr Lys Leu	
240 245 250	
aat acc acg gac cca agc agt gat gat gag gac ctc gca aca tcc ggc	819
Asn Thr Thr Asp Pro Ser Ser Asp Asp Glu Asp Leu Ala Thr Ser Gly	
255 260 265 270	
tca ggg tcc gga gaa cga gaa ccc cac aca act tct gat gcg gtc acc	867
Ser Gly Ser Gly Glu Arg Glu Pro His Thr Thr Ser Asp Ala Val Thr	
275 280 285	

aag	caa	ggg	ctt	tca	tca	aca	atg	cca	ccc	act	ccc	tca	cca	caa	cca	915
Lys	Gln	Gly	Leu	Ser	Ser	Thr	Met	Pro	Pro	Thr	Pro	Ser	Pro	Gln	Pro	
			290					295					300			
agc	acg	cca	cag	caa	gga	gga	aac	aac	aca	aac	cat	tcc	caa	gat	gct	963
Ser	Thr	Pro	Gln	Gln	Gly	Gly	Asn	Asn	Thr	Asn	His	Ser	Gln	Asp	Ala	
		305					310					315				
gtg	act	gaa	cta	gac	aaa	aat	aac	aca	act	gca	caa	ccg	tcc	atg	ccc	1011
Val	Thr	Glu	Leu	Asp	Lys	Asn	Asn	Thr	Thr	Ala	Gln	Pro	Ser	Met	Pro	
		320				325					330					
cct	cat	aac	act	acc	aca	atc	tct	act	aac	aac	acc	tcc	aaa	cac	aac	1059
Pro	His	Asn	Thr	Thr	Thr	Ile	Ser	Thr	Asn	Asn	Thr	Ser	Lys	His	Asn	
335					340					345					350	
ttc	agc	act	ctc	tct	gca	cca	tta	caa	aac	acc	acc	aat	gac	aac	aca	1107
Phe	Ser	Thr	Leu	Ser	Ala	Pro	Leu	Gln	Asn	Thr	Thr	Asn	Asp	Asn	Thr	
			355					360					365			
cag	agc	aca	atc	act	gaa	aat	gag	caa	acc	agt	gcc	ccc	tcg	ata	aca	1155
Gln	Ser	Thr	Ile	Thr	Glu	Asn	Glu	Gln	Thr	Ser	Ala	Pro	Ser	Ile	Thr	
			370					375					380			
acc	ctg	cct	cca	acg	gga	aat	ccc	acc	aca	gca	aag	agc	acc	agc	agc	1203
Thr	Leu	Pro	Pro	Thr	Gly	Asn	Pro	Thr	Thr	Ala	Lys	Ser	Thr	Ser	Ser	
		385				390						395				
aaa	aaa	ggc	ccc	gcc	aca	acg	gca	cca	aac	acg	aca	aat	gag	cat	ttc	1251
Lys	Lys	Gly	Pro	Ala	Thr	Thr	Ala	Pro	Asn	Thr	Thr	Asn	Glu	His	Phe	
		400				405					410					
acc	agt	cct	ccc	ccc	acc	ccc	agc	tcg	act	gca	caa	cat	ctt	gta	tat	1299
Thr	Ser	Pro	Pro	Pro	Thr	Pro	Ser	Ser	Thr	Ala	Gln	His	Leu	Val	Tyr	
415					420					425					430	
ttc	aga	aga	aag	cga	agt	atc	ctc	tgg	agg	gaa	ggc	gac	atg	ttc	cct	1347
Phe	Arg	Arg	Lys	Arg	Ser	Ile	Leu	Trp	Arg	Glu	Gly	Asp	Met	Phe	Pro	
			435					440					445			
ttt	ctg	gat	ggg	tta	ata	aat	gct	cca	att	gat	ttt	gac	cca	gtt	cca	1395
Phe	Leu	Asp	Gly	Leu	Ile	Asn	Ala	Pro	Ile	Asp	Phe	Asp	Pro	Val	Pro	
			450					455					460			
aat	aca	aaa	aca	atc	ttt	gat	gaa	tcc	tct	agt	tct	ggg	gcc	tcg	gct	1443
Asn	Thr	Lys	Thr	Ile	Phe	Asp	Glu	Ser	Ser	Ser	Ser	Gly	Ala	Ser	Ala	
		465					470					475				

gag gaa gat caa cat gcc tcc ccc aat att agt tta act tta tct tat	1491
Glu Glu Asp Gln His Ala Ser Pro Asn Ile Ser Leu Thr Leu Ser Tyr	
480 485 490	
ttt cct aat ata aat gag aac act gcc tac tct gga gaa aat gag aat	1539
Phe Pro Asn Ile Asn Glu Asn Thr Ala Tyr Ser Gly Glu Asn Glu Asn	
495 500 505 510	
gat tgt gat gca gag tta aga att tgg agc gtt cag gag gat gac ctg	1587
Asp Cys Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu	
515 520 525	
gcc gca ggg ctc agt tgg ata ccg ttt ttt ggc cct gga att gaa gga	1635
Ala Ala Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly	
530 535 540	
ctt tac act gct gtt tta att aaa aat caa aac aat ttg gtc tgc agg	1683
Leu Tyr Thr Ala Val Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg	
545 550 555	
ttg agg cgt cta gcc aat caa act gcc aaa tcc ttg gaa ctc tta ttg	1731
Leu Arg Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu	
560 565 570	
aga gtc aca act gag gaa aga aca ttc tcc tta atc aat aga cat gct	1779
Arg Val Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala	
575 580 585 590	
att gac ttt cta ctc aca aga tgg gga gga aca tgc aaa gtg ctt gga	1827
Ile Asp Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly	
595 600 605	
cct gat tgt tgc atc ggg ata gaa gac ttg tcc aaa aat att tca gag	1875
Pro Asp Cys Cys Ile Gly Ile Glu Asp Leu Ser Lys Asn Ile Ser Glu	
610 615 620	
caa att gac caa att aaa aag gac gaa caa aaa gag ggg act ggt tgg	1923
Gln Ile Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp	
625 630 635	
ggg ctg ggt ggt aaa tgg tgg aca tcc gac tgg ggt gtt ctt act aac	1971
Gly Leu Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn	
640 645 650	
ttg ggc att ttg cta cta tta tcc ata gct gtc ttg att gct cta tcc	2019
Leu Gly Ile Leu Leu Leu Leu Ser Ile Ala Val Leu Ile Ala Leu Ser	
655 660 665 670	

tgt att tgt cgt atc ttt act aaa tat atc gga taacgttaaa tgtgtaatga 2072
 Cys Ile Cys Arg Ile Phe Thr Lys Tyr Ile Gly
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ttaggacttt aggacaattg ctactgagcc c 2103

<210> 6

<211> 681

<212> PRT

<213> Marburg virus

<400> 6

Met Lys Thr Thr Cys Phe Leu Ile Ser Leu Ile Leu Ile Gln Gly Thr
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Lys Asn Leu Pro Ile Leu Glu Ile Ala Ser Asn Asn Gln Pro Gln Asn
 20 25 30

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
 35 40 45

Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
 50 55 60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
 65 70 75 80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
 85 90 95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Thr Asn
 100 105 110

Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
 115 120 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
130 135 140

Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
145 150 155 160

Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
165 170 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
180 185 190

Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
195 200 205

Thr Gly Cys Phe Gly Ala Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln
210 215 220

Thr Cys Ala Pro Ser Lys Ile Pro Pro Pro Leu Pro Thr Ala Arg Pro
225 230 235 240

Glu Ile Lys Leu Thr Ser Thr Pro Thr Asp Ala Thr Lys Leu Asn Thr
245 250 255

Thr Asp Pro Ser Ser Asp Asp Glu Asp Leu Ala Thr Ser Gly Ser Gly
260 265 270

Ser Gly Glu Arg Glu Pro His Thr Thr Ser Asp Ala Val Thr Lys Gln
275 280 285

Gly Leu Ser Ser Thr Met Pro Pro Thr Pro Ser Pro Gln Pro Ser Thr
290 295 300

Pro Gln Gln Gly Gly Asn Asn Thr Asn His Ser Gln Asp Ala Val Thr
305 310 315 320

Glu Leu Asp Lys Asn Asn Thr Thr Ala Gln Pro Ser Met Pro Pro His
 325 330 335

Asn Thr Thr Thr Ile Ser Thr Asn Asn Thr Ser Lys His Asn Phe Ser
 340 345 350

Thr Leu Ser Ala Pro Leu Gln Asn Thr Thr Asn Asp Asn Thr Gln Ser
 355 360 365

Thr Ile Thr Glu Asn Glu Gln Thr Ser Ala Pro Ser Ile Thr Thr Leu
 370 375 380

Pro Pro Thr Gly Asn Pro Thr Thr Ala Lys Ser Thr Ser Ser Lys Lys
 385 390 395 400

Gly Pro Ala Thr Thr Ala Pro Asn Thr Thr Asn Glu His Phe Thr Ser
 405 410 415

Pro Pro Pro Thr Pro Ser Ser Thr Ala Gln His Leu Val Tyr Phe Arg
 420 425 430

Arg Lys Arg Ser Ile Leu Trp Arg Glu Gly Asp Met Phe Pro Phe Leu
 435 440 445

Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr
 450 455 460

Lys Thr Ile Phe Asp Glu Ser Ser Ser Ser Gly Ala Ser Ala Glu Glu
 465 470 475 480

Asp Gln His Ala Ser Pro Asn Ile Ser Leu Thr Leu Ser Tyr Phe Pro
 485 490 495

Asn Ile Asn Glu Asn Thr Ala Tyr Ser Gly Glu Asn Glu Asn Asp Cys
 500 505 510

Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala
515 520 525

Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly Leu Tyr
530 535 540

Thr Ala Val Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg
545 550 555 560

Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val
565 570 575

Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp
580 585 590

Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp
595 600 605

Cys Cys Ile Gly Ile Glu Asp Leu Ser Lys Asn Ile Ser Glu Gln Ile
610 615 620

Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp Gly Leu
625 630 635 640

Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly
645 650 655

Ile Leu Leu Leu Leu Ser Ile Ala Val Leu Ile Ala Leu Ser Cys Ile
660 665 670

Cys Arg Ile Phe Thr Lys Tyr Ile Gly
675 680

<210> 7

<211> 25

<212> DNA

<213> Ross River virus

<400> 7
cgggatccac catgtctgcc gcgct

25

<210> 8

<211> 28

<212> DNA

<213> Ross River virus

<400> 8
cgctctagat taccgacgca ttggtatg

28